

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus.p2n model

Run on: December 12, 2002, 08:24:07 ; Search time 2 Seconds

(without alignments)
1.464 Million cell updates/sec

Title: us-09-371-347a-2

Perfect score: 3624

Sequence: 1 MRRFLLYATQGGAKAIAE.....AMKTLATLKEKRYLQDIWS 698

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1 seqs, 2097 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1 summaries

Command line parameters:

-MODEL=frame_plus.p2n.model -DEV=soft -Q=us-09-371-347a-2 -DB=us-09-371-347a-1
-SUFFIX=ptc -OUT=align_2_1 -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALLIGN=200
-THR_SCORE=ptc -THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=ptc
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLIFY
-NGC_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Database : us-09-371-347a-1.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3624	100.0	2097	1	us-09-371-347a-1

ALIGNMENTS

RESULT 1

us-09-371-347a-1

Alignment Scores:

Pred. No.:	0	Length:	2097
Score:	3624.00	Matches:	698
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	1	Gaps:	0

us-09-371-347a-2 (1-698) x us-09-371-347a-1 (1-2097)

Oy 1 MetArgPheLeuLeuLeuTyrAlaThrGlnGlnGlyClnAlaLysAlaLeaGlu 20

Db 1 ATGAGGAGGTTCTGTTACTATATGCTACAGCAGGAGGAGGCAAGGCCATCGCAGAA 60

Oy	21	GluMetCysGluGlnAlaValAlaHisGlyPheSerAlaAspLeuHisCysIleSerGlu 40
Db	61	GAATGTGTGAGCAAGCTGTGTACATGGATTTCTGCAGATCTTCACGTATTAGTGAA 120
Oy	41	SerAspLysTyrAspLeuLeuLysThrGluThrAlaProLeuValValValSerThrThr 60
Db	121	TCCGATAGTATGACCTAAACACCGAAACAGCTCTCTTGTGTGTGTGTCTTACCACG 180
Oy	61	GlyThrGlyAspProAspThrAlaArgLysPheValLysGluLleGlnAsnGlnThr 80
Db	181	GGCACCGGAGACCCACCGCACACAGCTTGTGTAAAGGAAATACACAAACCAACA 240
Oy	81	LeuProValAspPheAlaHisLeuArgTyrGlyLeuLeuGlyLeuGlyAspSerGlu 100
Db	241	CTGCCCGGTGATTTCTTCTCCTCCCTGCGGTATGGTCTCGGTGATTCAGAA 300
Oy	101	TyrThrTyrPheCysAsnGlyGlyLysIleAspLysArgLeuGlnGluLeuGlyAla 120
Db	301	TACACCTACTTTTGCATGGGGGGAAGATAATTTGATTAACGACTTTCAAGAGCTTGGAGCC 360
Oy	121	ArgHisPheTyrAspThrGlyHisAlaAspAspCysValGlyLeuGluLeuValValGlu 140
Db	361	CGGCATTTCTATGACACTGGACATGGCAGATGACTGTGTAGGTTTAGAACTTTGTGTTGAG 420
Oy	141	ProTyrPheAlaGlyLeuTyrProAlaLeuArgLysHisPheArgSerArgGlyGln 160
Db	421	CCGTGGATTGCTGACTCTGCCAGCCCTCAGAAAGCATTTTAGGTCAAGCAGAGGACAA 480
Oy	161	GluGluLeuSerGlyAlaLeuProValAlaSerProAlaSerLeuArgThrAspLeuVal 180
Db	481	GAGGAGATAAGTGGCGCCTCCCGGTGGCATCCTGCATCCTTGAGGACAGACTTGTG 540
Oy	181	LysSerGluLeuLeuHisIleGluSerGlnValGluLeuLeuArgPheAspAspSerGly 200
Db	541	AGTCAGAGCTGCTACACATGAAATCTCAAGTCGACTTCTCAGATTTCGATGATTCAGGA 600
Oy	201	ArgLysAspSerGluValLeuLysGlnAsnAlaValAsnSerAsnGlnSerAsnValVal 220
Db	601	AGAAAGGATTTCTGAGGTTTCAAGCAAAATGCAAGTGAACAGCAACCAATCCAAATGTTGTA 660
Oy	221	IleGluAspPheGluSerSerLeuThrArgSerValProProLeuSerGlnAlaSerLeu 240
Db	661	ATTGAAGACTTTGAGTCTCTCCTACTTACCCGTTCCGTTACCCCTCTCAAGCTCTCTG 720
Oy	241	AsnIleProGlyLeuProGluTyrLeuGlnValHisLeuGlnGluSerLeuGlyGln 260
Db	721	AATATCTCTGTTTACCCCGCAGAAATATTTACAGGTACATCTCGAGGAGTCTCTTGGCCAG 780
Oy	261	GluGluSerGlnValSerValThrSerAlaAspProValPheGlnValProIleSerLys 280
Db	781	GAGGAAAGCCCAAGTATCTGTGACTTCAGCAGATCCAGTTTTCAGAGTCCCAATTTCAAAG 840
Oy	281	AlaValGlnLeuThrThrAsnAspAlaIleLysThrThrLeuLeuValGluLeuAspIle 300
Db	841	GCAGTTCAACTTACTACGAATGATGCCATAAACCACTCTCTGCTGATAGATTGGACATT 900
Oy	301	SerAsnThrAspPheSerTyrGlnProGlyAspAlaPheSerValIleCysProAsnSer 320
Db	901	TCAAATACAGACTTTTCTATCAGCTCGAGATGCCCTTCAGCGTGATCTGCGCTTAACAGT 960
Oy	321	AspSerGluValGlnSerLeuLeuGlnArgLeuGlnLeuGluAspLysArgGluHisCys 340
Db	961	GATTCGTGAGGTACAAAGCCTTACTCCAAAGACTCCAGCTTGAAGATAAAGAGACGACTGC 1020
Oy	341	ValLeuLeuLysIleLysAlaAspThrLysLysGlyAlaThrLeuProGlnHisIle 360
Db	1021	GTCCCTTTTGAATAAAGGCGACACAAAGAAAGGAGGTACCTTACCCCGACATATA 1080
Oy	361	ProAlaGlyCysSerLeuGlnPheIlePheThrTrpCysLeuGluIleArgAlaIlePro 380
Db	1081	CCTCGGGATGTTCTCTCCAGTTTCATTTTACCTGTGTCTTGAATCCGAGCAATTCCT 1140

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Oy 381 LysLysAlaPheLeuArgAlaLeuValAspTyrThrSerAspSerAlaGluLysArgArg 400
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Db 1141 AAAAGGCATTTTGGAGCCCTTGTGACTATACCACTGACAGTGTGAAAAGCCAGG 1200

Oy 401 LeuGlnGluLeuCysSerLysGlnGlyAlaAlaAspTyrSerArgPheValArgAspAla 420
|||||
Db 1201 CTACAGAGCTGTGAGTAAACAGAGGACCCGATATAGCCGCTTGTACGAGATGCC 1260

Oy 421 CysAlaCysLeuLeuAspLeuLeuAlaPheProSerCysGlnProProLeuSerLeu 440
|||||
Db 1261 TGTGCCCTGTGTGTGGATCTCTCTGCTTTCCTTCTTCCAGGACCCAGCTCAGTCTC 1320

Oy 441 LeuLeuGluHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerLeu 460
|||||
Db 1321 CTGCTCGAACATCTTCTAAACTTCAACCCAGACCATATTCTGTGTCAGCTCAAGTTTA 1380

Oy 461 PheHisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThr 480
|||||
Db 1381 TTTACCCAGGAAGCTCTCTTTGTCTCAACATTTGGAATTTCTGCTACTGCCACA 1440

Oy 481 ThrGluValLeuArgLysGlyValCysThrGlyTrpLeuAlaLeuLeuValAlaSerVal 500
|||||
Db 1441 ACAGAGGTTCTCGGAAGGGAGTATGTACAGGCTGGCTGCTTGTGTGCTTCAAGTT 1500

Oy 501 LeuGlnProAsnIleHisAlaSerHisGluAspSerGlyLysAlaLeuAlaProLysIle 520
|||||
Db 1501 CTTCAGGCAACATACATGCTATCCATGACAGACGCGGAAAGCCCTGCTCCTAAGATA 1560

Oy 521 SerIleSerProArgThrThrAsnSerPheHisLeuProAspSerProSerIleProIle 540
|||||
Db 1561 TCCATCTCTCCCGAACACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCCATC 1620

Oy 541 IleMetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgGlu 560
|||||
Db 1621 ATAATGGTGGTCCAGGAACCGCATAGCCCGTTTATTGGGTTCTTACACATAGAGAG 1680

Oy 561 LysLeuGlnGluHisProAspGlyAsnPheGlyAlaMetTrpLeuPhePheGlyCys 580
|||||
Db 1681 AAACCTCAGAACACACCCAGATGGAATTTGGAGCAATGGTGTGTTTTTGGCTGC 1740

Oy 581 ArgHisLysAspArgAspTyrLeuPheArgLysGluLeuArgHisPheLeuLysHisGly 600
|||||
Db 1741 AGGCATAAGGATAGGATTTATCTATTCAAGAAAGAGCTCAGACATTTCTTAAAGCATGG 1800

Oy 601 IleLeuThrHisLeuLysValSerPheSerArgAspAlaProValGlyGluGluAla 620
|||||
Db 1801 ATCTTAACATCATTAAGGTTTCTTCTCAAGAGATGCTCTGTGGGAGGAGGAGGCC 1860

Oy 621 ProAlaLysTyrValGlnAspAsnIleGlnLeuHisGlyGlnGlnValAlaArgIleLeu 640
|||||
Db 1861 CCAGCAAGATATGTACAAGACAACTCCAGCTTCATGCCAGCAGGTGGCGAGAATCCTC 1920

Oy 641 LeuGlnGluAsnGlyHisIleTyrValCysGlyAspAlaLysAsnMetAlaLysAspVal 660
|||||
Db 1921 CTCAGGAGAACCGCCATATTTATGTGTGGAGATGCAAGAAATATGGCCAAGGATGA 1980

Oy 661 HisAspAlaLeuValGlnIleIleSerLysGlnValGlyValGluLysLeuGluAlaMet 680
|||||
Db 1981 CATGATGCCCTTGTGCAATAATAAGCAAGAGGTGGAGTTGAAAACCTAGAACCAATG 2040

Oy 681 LysThrLeuAlaThrLeuLysGluLysArgTyrLeuGlnAspIleTrpSer 698
|||||
Db 2041 AAAACCTGSCCACTTAAAGAGAGAAAACGCTACCTTCAGGATATTTGGTCA 2094
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Search completed: December 12, 2002, 08:24:13
Job time : 6 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 12, 2002, 08:25:56 ; Search time 2 Seconds
(without alignments)
1.464 Million cell updates

Title: us-09-371-347a-42
 Perfect score: 3623
 Sequence: 1 MRRELLLVATQGGQAKAIAE.....AMKTLATLKEERYLQDINS 698

Scoring table:	BLOSUM62		
Xgapop	10.0	Xgapext	0.1
Ygapop	10.0	Ygapext	0.1
Fgapop	6.0	Fgapext	0.1
Delop	6.0	Delext	0.1

Searched: 1 seqs, 2097 residues

Total number of hits satisfying chosen parameters: 2

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0
                  Maximum Match 10
                  Listing first 15

```

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Command line parameters:
MODEL=frame; p2m=model; DEV=soft; Qrus=09-371-347a-42; DB=us-09-371-347a-41
SUFFIX=plc; Out=align_42_41; MINMATCH=0; LOOPC=0; LOOPEXT=0; UNITS=bits
START=1; END=1; MATRIX=plcsmc62; TRANS=human40; cdi; LST=1; LOCALTGM=200
THR SCORE=pcr; THR MAX=100; THR MIN=0; ALIGN=1; MODE=LOCAL; OUT=plc
NORM=acc; HPA32=500; MINLEN=0; MAXLEN=200000000; NCPU=6; NO.XLIFY
NEG SCORES=0; LONGLOG; THREADS=1; XGAPO=10; XGAPO=6; XGAPO=6
XGAPOEXT=0.1; XGAPO=10; XGAPOEXT=0.1; DELOP=6; DELEX=0.1

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Database : us-09-371-347a-41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	3623	100.0	2097	1	us-09-371-347a-41

ALIGNMENTS

RESULT 1
US-09-371-347a-41

Alignment Scores:
Pred. No.:
Score:
Percent Similarity:
Best Local Similarity:
Query Match:
DB:

us-09-371-347a-42 (1-698) x us-09-371-347a-41 (1-2097)

Qy 1 MetArgArgPheLeuLeuLeuTyrAlaThrGlnGlnGlyGlnAlaLysAlaIleAlaGlu 20
Dd 1 ATGAGGAGGTTCCTGTTACTATATGCTACACAGCGGGACAGGCCAAGSCCATCGCAGA 60	

```
Oy 381 LysLysAlaPheLeuArgAlaLeuValAspTyrThrSerAspSerAlaGluLysArgAtg 400
Db 1141 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Oy 401 LeuGlnGluLeuCysSerLysGlnGlyAlaAlaAspTyrSerArgPheValArgAspAla 420
Db 1201 CTACAGAGCTGTGCAGTAACAAAGGGCAGCCGATTATAGCCGCTTTGTACGAGATGCC 1260
Oy 421 CysAlaCysLeuLeuAspLeuLeuLeuAlaPheProSerCysGlnProProLeuSerLeu 440
Db 1261 TGTGCTGTCTGTGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC 1320
Oy 441 LeuLeuGluHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerLeu 460
Db 1321 CTGCTGAACATCTTCTAACTTCAACCCAGACCATATCTGTGCAAGCTCAAGTTTA 1380
Oy 461 PheHisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThr 480
Db 1381 TTTCACCCAGAAAGCTCCATTTTCTTCAACATTTGTGGAATTTCTGTCTACTGCCACA 1440
Oy 481 ThrGluValLeuArgLysGlyValCysThrGlyTrpLeuAlaLeuValAlaSerVal 500
Db 1441 ACAGAGTTCTCGGAAGGAGATGTACAGGCTGGCTGGCTGTGTGGTTGCTTCAGTT 1500
Oy 501 LeuGlnProAsnIleHisAlaSerHisGluAspSerGlyLysAlaLeuAlaProLysIle 520
Db 1501 CTTACGCCAAACATACATCCATCCATGAACACAGCGGAAAGCCCTGGCTCCTTAAGATA 1560
Oy 521 SerIleSerProArgThrThrAsnSerPheHisLeuProAspAspProSerIleProIle 540
Db 1561 TCCATCTCTCTCGAACAATAATCTTTCCACTTACCAGATGACCCCTCAATCCCCATC 1620
Oy 541 IleMetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgGlu 560
Db 1621 ATATGCTGGTCCAGAACCCGGCATAGCCCGTTTATGGTTCTTACACATAGAGAG 1680
Oy 561 LysLeuGlnGluHisProAspGlyAsnPheGlyAlaMetTrpLeuPhePheGlyCys 580
Db 1681 AAATCCCAAGAACACCCAGATGGAATTTTGGAGCAATGTGTTGTTTTTGGCTGC 1740
Oy 581 ArgHisLysAspArgAspTyrLeuPheArgLysGluLeuArgHisPheLeuLysHisGly 600
Db 1741 AGGCATAAGCATAGGCATTATCTATTCAGAAAGAGCTCACACATTTCTTAAGCATGGG 1800
Oy 601 IleLeuThrHisLeuLysValSerPheSerArgAspAlaProValGlyGluGluAla 620
Db 1801 ATCTTAACCTCATTAAGTTTCTTCTCAAGAGATGCTCTCTTGGGGAGGAGGAGCC 1860
Oy 621 ProAlaLysTyrValGlnAspAsnIleGlnLeuHisGlyGlnValAlaArgIleLeu 640
Db 1861 CCAGCAAAAGTATGTACAAGACAACATCCAGCTTCATGCCAGCAGGTGGCGAGAACTCTC 1920
Oy 641 LeuGlnGluAsnGlyHisIleTyrValCysGlyAspAlaLysAsnMetAlaLysAspVal 660
Db 1921 CTCCAGGAGAACCGCCATATTATGTGTGGAGATGCCAAGAATATGGCCAGGATGTA 1980
Oy 661 HisAspAlaLeuValGlnIleIleSerLysGluValGlyValGluLysLeuGluAlaMet 680
Db 1981 CATGATGCCCTTGTGCAAAATAATAGCAAGAGAGTTGGAGTTGAAAACTAGAACCAATC 2040
Oy 681 LysThrLeuAlaThrLeuLysGluLysArgTyrLeuGlnAspIleTrpSer 698
Db 2041 AAACCCCTGGCCACTTTTAAAGAGAAGAAACCGCTACCTTCAGGATATTGGTCA 2094
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Search completed: December 12, 2002, 08:26:03
Job time : 7 secs


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QY 381 LysLysAlaPheLeuArgAlaLeuValAspTyrThrSerAspSerAlaGluLysArg 400
Db 1141 AAAAAAGGCATTTTGGAGGCCCTTGTGGACTATACAGTGCACAGTCTCAAAAGCCAGG 1200
QY 401 LeuGlnGluLeuCysSerLysGlnGlyValAlaAspTyrSerArgPheValArgAspAla 420
Db 1201 CTACAGGAGCTGTGCAGTAAACAAGGGCAGCCGATATAGCCGCTTTGTACGAGATGCC 1260
QY 421 CysAlaCysLeuLeuAspLeuLeuAlaPheProSerCysGlnProProLeuSerLeu 440
Db 1261 TGTGGCTGCTTGTGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
QY 441 LeuLeuGluHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerLeu 460
Db 1321 CTGCTCGAACATCTTCCCTAACTTCAACCCAGACCATATTCTGTCGCAAGCTCAAGTTTA 1380
QY 461 PheHisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThr 480
Db 1381 TTTCACCCAGGAAGCTCCATTTTGTCTTCAACATTTGTGAATTTCTGTCTACTGCCACA 1440
QY 481 ThrGluValLeuArgLysGlyValCysThrGlyTrpLeuAlaLeuValAlaSerVal 500
Db 1441 ACAGAGGTTCTCGGAAGGGAGTATGTACAGGCTGGCTGGCTTGTGGTTCAGTT 1500
QY 501 LeuGlnProAsnIleHisAlaSerHisGluAspSerClyLysAlaLeuAlaProLysIle 520
Db 1501 CTTACGCCAANACATACATGCATCCATGACAGACAGCGGAAAGCCCTGGCTCTAGATA 1560
QY 521 SerIleSerProArgThrThrAsnSerPheHisLeuProAspAspProSerIleProIle 540
Db 1561 TCCATCTCTCTCTCGAACACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCCATC 1620
QY 541 IleMetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgGlu 560
Db 1621 ATAATGGTGGGTCCAGGAACCGCATAGCCCGTTTATTTGGTTCTCTACAACATAGAGAG 1680
QY 561 LysLeuGlnGluGlnHisProAspGlyAsnPheClyAlaMetTrpLeuPhePheGlyCys 580
Db 1681 AACTCCAAAGAACACACCCAGATGGAAATTTGGAGCAATGGTGTGTTTTTGGCTGC 1740
QY 581 ArgHisLysAspArgAspTyrLeuPheArgLysGluLeuArgHisPheLeuLysHisGly 600
Db 1741 AGGCATAAGGATAGGGATATCTATTTCAGAAAAGAGCTCAGACATTTCTTAAAGCATGGG 1800
QY 601 IleLeuThrHisLeuLysValSerPheSerArgAspAlaProValGlyGluGluAla 620
Db 1801 ATCTTAACATCATCTAAGGTTTCTTCTCAAGAGATGCTCTCTGGGAGGAGGAGGCC 1860
QY 621 ProAlaLysTyrValGlnAspAsnIleGlnLeuHisGlyGlnValAlaArgIleLeu 640
Db 1861 CCAGCAAGATATGTACAAGACAACTCCAGCTTCATGCCAGCAGGTGGCGAGAATCTCTC 1920
QY 641 LeuGlnGluAsnGlyHisIleTyrValCysGlyAspAlaLysAsnMetAlaLysAspVal 660
Db 1921 CTCAGGACAGCGGCATATTTATGTGTGTGGAGATCCAAAGATATGGCCAGGATGTA 1980
QY 661 HisAspAlaLeuValGlnIleIleSerLysGluValGlyValGluLysLeuGluAlaMet 680
Db 1981 CATGATGCCCTTGTGCAAAATAAAGCAAGAGGTTGGAGTTGAAAACCTAGAACCAATG 2040
QY 681 LysThrLeuAlaThrLeuLysGluLysArgTyrLeuGlnAspIleTrpSer 698
Db 2041 AAAACCTGGCCACTTAAAGAGAAAAACGCTTACCTTCAGGATATTTGGTCA 2094
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Search completed: December 12, 2002, 08:27:19
Job time : 7 secs


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Qy 381 LysLysAlaPheLeuArgAlaLeuValAspTyrThrSerAspSerAlaGluLysArg 400
Db 1141 AAAAAAGGCAATTTTTCGAGCCCTTGTGGACTATACAGTGCACAGTCTGAAAAAGCCAGG 1200
Qy 401 LeuGlnGluLeuCysSerLysGlnGlyAlaAlaAspTyrSerArgPheValArgAspAla 420
Db 1201 CTACAGGAGCTGTGCAGTAAACAGGGGCGAGCGATTATAGCGCTTGTACAGATGCC 1260
Qy 421 CysAlaCysLeuLeuAspLeuLeuAlaPheProSerCysGlnProProLeuSerLeu 440
Db 1261 TGTGGCTGCTGTGTGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
Qy 441 LeuLeuGluHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerLeu 460
Db 1321 CTGCTCGAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1380
Qy 461 PheHisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThr 480
Db 1381 TTTCACCCAGGAAGCTCCATTTTGTCTTCAACATTGTGGAAATTTCTGTCTACTGCCACA 1440
Qy 481 ThrGluValLeuArgLysGlyValCysThrGlyTyrPheLeuAlaLeuValAlaSerVal 500
Db 1441 ACAGAGGTTCTCGGAAGGGAGTATGACAGGTGGCTGGCTTGTGGTGTCTTCAAGTT 1500
Qy 501 LeuGlnProAsnIleHisAlaSerHisGluAspSerGlyLysAlaLeuAlaProLysIle 520
Db 1501 CTTACGCCAAACATACATGCATCCATGAACAGACGGGAAACCCCTGGCTCCTAAGATA 1560
Qy 521 SerIleSerProArgThrThrAsnSerPheHisLeuProAspAspProSerIleProIle 540
Db 1561 TCCATCTCTCTCTCGAACAACAAATTTCTTCCACTTACAGATGACCCCTCAATGCCCATC 1620
Qy 541 IleMetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgGlu 560
Db 1621 ATAATGTTGGTCCAGGAACCGGATAGCCCGTTTATTGGGTTCTTACAACATAGAGAG 1680
Qy 561 LysLeuGlnGluGlnHisProAspGlyAsnPheGlyAlaMetTyrPhePheGlyCysArg 580
Db 1681 AAATCCAGAACACACACCCAGTGGAAATTTGGACAAATGGGTTTTTGGCTGCAGG 1740
Qy 581 HisLysAspArgAspTyrLeuPheArgLysGluLeuArgHisPheLeuLysHisGlyIle 600
Db 1741 CATAAGGATAGGATTTATCTATTTCAGAAAGAGCTCAGACATTTCTCTTAAGCATGGATC 1800
Qy 601 LeuThrHisLeuLysValSerPheSerArgAspAlaProValGlyGluGluAlaPro 620
Db 1801 TTAATCATCTAAGGTTTCTCTCTCAAGAGATGCTCTCTTGGGAGGAGGAGGCCCA 1860
Qy 621 AlaLysTyrValGlnAspAsnIleGlnLeuHisGlyGlnGlnValAlaArgIleLeuLeu 640
Db 1861 GCAAAGTATGTACAAGACAACTCCAGCTTCATGGCCAGCAGGTGGCGAATCTCTCTC 1920
Qy 641 GlnGluAsnGlyHisIleTyrValCysGlyAspAlaLysAsnMetAlaLysAspValHis 660
Db 1921 CAGGAGAACGGCCATATTTATGTGTGGAGATGCAAGAAATATGGCCAAAGGATGTACAT 1980
Qy 661 AspAlaLeuValGlnIleIleSerLysGluValGlyValGluLysLeuGluAlaMetLys 680
Db 1981 GATGCCCTTGTGCAATATATAGCAAGAGGTTGGAGTTGNAANAACATAGAGCAATGAAA 2040
Qy 681 ThrLeuAlaThrLeuLysGluLysArgTyrLeuGlnAspIleTyrPheSer 697
Db 2041 ACCCTGGCCACTTTAAAGAGAAAAACGCTACCTTCAGGATATTTGGTCA 2091
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Search completed: December 12, 2002, 08:28:29
Job time : 4 secs

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 12, 2002, 08:29:25 ; Search time 1 Seconds
(without alignments)
2.884 Million cell updates/sec

Title: us-09-371-347a-48
Perfect score: 3568
Sequence: 1 RRELLYATQGOAKAIAEE.....NKQRPWLKKKNATFRIFGH 689

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.1
Ygapop 10.0 , Ygapext 0.1
Fgapop 6.0 , Fgapext 0.1
Delop 6.0 , Delext 0.1

Searched: 1 seqs, 2093 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=soft -Q=us-09-371-347a-48 -DB=us-09-371-347a-47
-SUFFIX=ptc -OUT=align_48_47 -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits
-START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=1 -DOCALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT=ptc
-NORM=exc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -NCPU=6 -NO_XLPHY
-NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -Fgapop=6
-Fgapext=0.1 -Ygapop=10 -Ygapext=0.1 -DELOP=6 -DELEXT=0.1

Database : us-09-371-347a-47.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	DB ID	Description
1	3529.9	98.9	2093	1 us-09-371-347a-47

ALIGNMENTS

RESULT 1
us-09-371-347a-47

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
0	3529.90	97.04%	97.04%	98.93%	1	2093	589	0	21	0	

us-09-371-347a-48 (1-689) x us-09-371-347a-47 (1-2093)

Qy 1 ArgArgPheLeuLeuTyrAlaThrGlnGlnGlyGlnAlaLysAlaLleAlaGluGlu 20
Db 4 AGGAGGTTCTGTCTACTATATCTACACAGCAGGGGACAGCAAGGCCATCGCAGAAGAA 63

Qy	21	MetCysGluGlnAlaValAlaHisGlyPheSerAlaAspLeuHisCysIleSerGluSer	40
Db	64	ATGTGTGAGCAAGCTGTGTACATGGATTTCTGCAGATCTTCACTGTATTAGTGNATCC	123
Qy	41	AspLysTyrAspLeuLysThrGluThrAlaProLeuValValValSerThrThrGly	60
Db	124	GATAAGTATGACCTAAACCAACGAAACAGCTCTCTTGTGTGTGTCTTACCACGGCC	183
Qy	61	ThrGlyAspProAspThrAlaArgLysPheValLysGluIleGlnAsnGlnThrLeu	80
Db	184	ACCGAGACCCACCCGACACAGCCGCAAGTTTGTAAAGGAAATACACAAACCAACTG	243
Qy	81	ProValasPhePheAlaHisLeuArgTyrGlyLeuLeuGlyLeuGlyAspSerGluTyr	100
Db	244	CCGGTGTATTTCTTGTCTACCTCGGTATGGGTACTGGGTCTCGGTATTCAGAAATAC	303
Qy	101	ThrTyrPheCysAsnGlyGlyLysIleLeuAspLysArgLeuGlnGluLeuGlyAlaArg	120
Db	304	ACCTACTTTTGCATGGGGGGAAGATAAATGATAAAGCACTTCAAGAGCTTGGAGCCGG	363
Qy	121	HisPheTyrAspThrGlyHisAlaAspAspCysValGlyLeuGluLeuValValGluPro	140
Db	364	CATTTCTATGACACTGGACATGCAGATGACTGTGTAGGTTTAAACTTGTGGTTGAGCCG	423
Qy	141	TrpIleAlaGlyLeuTrpProAlaLeuArgLysHisPheArgSerArgGlyGlnGlu	160
Db	424	TGGATTGCTGGACTCTGCCAGCCCTCAGAAAGCATTTTAGGTCAAGCAGAGCAAGAG	483
Qy	161	GluIleSerGlyAlaLeuProValAlaSerProAlaSerLeuArgThrAspLeuValLys	180
Db	484	GAGATAACTGGCGCACCTCCCGTGGCATCATCTGCATCTCTGAGCAGACAGCTTGTCAAG	543
Qy	181	SerGluLeuLeuHisIleGlySerGlnValGluLeuLeuArgPheAspSerGlyArg	200
Db	544	TCAGAGCTGCTACACATTTGAATCTCAAGTCGAGCTCTCGAGATTCTGATTCAGAGAAGA	603
Qy	201	LysAspSerGluValLeuLysGlnAsnAlaValAsnSerAsnGlnSerAsnValIle	220
Db	604	AAGGATTCAGAGTTTGAACCAAAATGCAGTGAACAGCAACCAATCCCAATGTTGTAAT	663
Qy	221	GluAspPheGluSerLeuThrArgSerValProProLeuSerGlnAlaSerLeuAsn	240
Db	664	GAAGACTTTGAGTCTCTACCTTACCCGTTCCGTTACCCCACTCTCACAGCTCTCTGAAT	723
Qy	241	IleProGlyLeuProProGluTyrLeuGlnValHisLeuGlnGlnSerLeuGlyGlnGlu	260
Db	724	ATTCTGTGTTTACCCCAAGAAATATTACAGGTACATCTCGAGGAGTCTCTTGGCCAGAG	783
Qy	261	GluSerGlnValSerValThrSerAlaAspProValPheGlnValProIleSerLysAla	280
Db	784	GAAGCCAAGTATCTGTGACTTTCAGCAGATCCAGTTTTCAAAGTCCCAATTTCAAGGCA	843
Qy	281	ValGlnLeuThrThrAsnAspAlaIleLysThrThrLeuValValGluLeuAspIleSer	300
Db	844	GTTCAACTTACTAGCATGATGATGCCATTAACCACTCTCTGTGTAGATTGGACATTTCA	903
Qy	301	AsnThrAspPheSerTyrGlnProGlyAspAlaPheSerValIleCysProAsnSerAsp	320
Db	904	AAATACAGACTTTTCTCTATCAGCTTGGAGATGCTTTCAGCGTGTATCTGCCCTAACAGTAT	963
Qy	321	SerGluValGlnSerLeuLeuGlnArgLeuGlnLeuAspLysArgGluHisCysVal	340
Db	964	TCTGAGGTACAAAGCCTACTCCAAAGACTCGACTTGAAGATTAAGAGAGGAGCTGCCGC	1023
Qy	341	LeuLeuLysIleLysAlaAspThrLysLysGlyAlaThrLeuProGlnHisIlePro	360
Db	1024	CTTTTGAATAAAGGGCAGACACAAAGAAAGAGGAGCTACCTTACCCCAAGCATATACCT	1083
Qy	361	AlaGlyCysSerLeuGlnPheIlePheThrTrpCysLeuGluIleArgAlaIleProLys	380
Db	1084	CGGGGATGTTCTCTCCAGTTTCATTTTACCTGTGTCTTGAATCCGAGCAATTCCTAAA	1143

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QY 381 LysAlaPheLeuArgAlaLeuValAspTyrThrSerAspSerAlaGluLysArgLeu 400
    |||||
Db 1144 AAGGCATTTTGGAGCCCTTGTGGACTATACCAGTGCAGTCTGAAAGCGCAGGCTA 1203
QY 401 GlnGluLeuCysSerLysGlnGlyValAlaAspTyrSerArgPheValArgAspAlaCys 420
    |||||
Db 1204 CAGGAGCTGTGCAGTAAACAGGGGAGCCGATATAGCCGCTTTGTAGAGATGCCCTGT 1263
QY 421 AlaCysLeuLeuAspLeuLeuAlaPheProSerCysGlnProProLeuSerLeuLeu 440
    |||||
Db 1264 GCCTGCTTGTGGATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTG 1323
QY 441 LeuGluHisLeuProLysLeuGlnProArgProTyrSerCysAlaSerSerLeuPhe 460
    |||||
Db 1324 CTCGAACATCTTCTTAACCTTCAACCCAGACCATATTCGTGTGCAAGCTCAAGTTTATT 1383
QY 461 HisProGlyLysLeuHisPheValPheAsnIleValGluPheLeuSerThrAlaThrThr 480
    |||||
Db 1384 CACCAGGAAAGCTCCATTTTGTCTTCAACATTGTGGAATTTCTGTCTACTGCCACAACA 1443
QY 481 GluValLeuArgLysGlyValCysThrGlyTrpLeuAlaLeuValAlaSerValLeu 500
    |||||
Db 1444 GAGGTTCTCGGAGGAGGATGTACAGGCTGGCTGGCTTGTGTGCTTCAAGTCTCT 1503
QY 501 GlnProAsnIleHisAlaSerHisGluAspSerGlyLysAlaLeuAlaProLysIleSer 520
    |||||
Db 1504 CAGCCAAACATACATGCATCCCATGAGACAGCGGGAAGCCCTGCTCTAAGATATCC 1563
QY 521 IleSerProArgThrThrAsnSerPheHisLeuProAspAspProSerIleProIleIle 540
    |||||
Db 1564 ATCTCTCTCGAACAAACAAATCTTCTTCCACTTACAGATGACCCCTCAATCCCATCAT 1623
QY 541 MetValGlyProGlyThrGlyIleAlaProPheIleGlyPheLeuGlnHisArgAsnSer 560
    |||||
Db 1624 ATGGTGGGTCCAGGAACCGCATAGCCCGTTTATTGGGTCTCTACAAACATAGAACTCC 1683
QY 561 LysAsnAsnThrGluMetGluIleLeuGluCysGlyCysPheLeuAlaGlyIle 580
    |||||
Db 1684 AAGAACAACCCCATGGAATTTTGGAGCAATGTGGTTGTTTGGCTGCAGGCATA 1743
QY 581 ArgIleGlyIleIleTyrSerGluLysSerSerAspIleSerLeuSerMetGlySer--- 599
    |||||
Db 1744 AGGATAGGGATTATCTATTGAAAGAGCTCAGACATTTCTTAAGCATGGGATCTTAA 1803
QY 600 LeuIle---ArgPheProSerGlnGluMetLeuLeuLeuGlyArgArgLysProGlnGln 618
    |||||
Db 1804 CTCATCTAAGGTTTCTCTCTCAGAGATGCTCTGTGGGAGAGGAGGCCAGCAA 1863
QY 619 SerMetTyrLysThrThrSerSerPheMetAlaSerArgTrpArgLysSerSerArg 638
    |||||
Db 1864 AGTATGTACAGACAAACATCCAGCTTTCATGGCCAGCAGGTGGCGGAGAAATCCTCTCCAGG 1923
QY 639 ArgThrAlaIlePheMetCysValGluMetGlnArgIleTrpProArgMetTyrMetMet 658
    |||||
Db 1924 AGAAGCCCATATTATGTGTGTGGAGATGCAAGAAATATGGCCAGGATGTACATGATG 1983
QY 659 ProLeuCysLys-----AlaLysArgLeuLeuLysAsn---LysGln---LysPro 674
    |||||
Db 1984 CCCTTGTGCAATAATAAGCAAGAGGTGGAGTTGAAAACTAGAAAGCAATGAAACCC 2043
QY 675 TrpProLeu---LysLysLysAsnAlaThrPheArgIlePheGlyHis 689
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Db 2044 TGCCCACTTTAAAGAGAAAGAAACGCTACCTTCAGGATATTGGTCAAT 2091
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Search completed: December 12, 2002, 08:29:31
Job time : 6 secs